

## SEQUENCE LISTING

caa atc ctg ggt gtc aaa gcc tct agg ttt ctt tgc caa cag cca gat 337  
Gln Ile Leu Gly Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp

[illegible]

95 100 105

gga gct ctc tat gga tcg cct cac ttt gat cct gag gcc tgc agc ttc 385  
 Gly Ala Leu Tyr Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe  
 110 115 120

aga gaa ctg ctg ctg gag gac ggt tac aat gtg tac cag tct gaa gcc 433  
 Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala  
 125 130 135 140

cat ggc ctg ccc ctg cgt ctg cct cag aag gac tcc cca aac cag gat 481  
 His Gly Leu Pro Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp  
 145 150 155

gca aca tcc tgg gga cct gtg cgc ttc ctg ccc atg cca ggc ctg ctc 529  
 Ala Thr Ser Trp Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu  
 160 165 170

cac gag ccc caa gac caa gca gga ttc ctg ccc cca gag ccc cca gat 577  
 His Glu Pro Gln Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp  
 175 180 185

gtg ggc tcc tct gac ccc ctg agc atg gta gag cct tta cag ggc cga 625  
 Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg  
 190 195 200

agc ccc agc tat gcg tcc tga ctcttctga atc 659  
 Ser Pro Ser Tyr Ala Ser \*  
 205 210

<210> 2  
 <211> 210  
 <212> PRT  
 <213> Mus musculus

<400> 2  
 Met Glu Trp Met Arg Ser Arg Val Gly Thr Leu Gly Leu Trp Val Arg  
 1 5 10 15  
 Leu Leu Leu Ala Val Phe Leu Leu Gly Val Tyr Gln Ala Tyr Pro Ile  
 20 25 30  
 Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg  
 35 40 45  
 Tyr Leu Tyr Thr Asp Asp Asp Gln Asp Thr Glu Ala His Leu Glu Ile  
 50 55 60  
 Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser Pro Glu Ser  
 65 70 75 80  
 Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly  
 85 90 95  
 Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly Ala Leu Tyr  
 100 105 110  
 Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu  
 115 120 125  
 Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro

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130	135	140
Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala Thr Ser Trp		
145	150	155
Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His Glu Pro Gln		160
	165	170
Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val Gly Ser Ser		175
	180	185
Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg Ser Pro Ser Tyr		190
	195	200
Ala Ser		205
210		

<210> 3  
 <211> 643  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (9)...(638)

<400> 3  
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           Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp  
           1                          5                          10

gtt tct gtg ctg gct ggt ctt ctg ctg gga gcc tgc cag gca cac ccc 98  
 Val Ser Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro  
   15                          20                          25                          30

atc cct gac tcc agt cct ctc ctg caa ttc ggg ggc caa gtc cgg cag 146  
 Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln  
                           35                          40                          45

cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc cac ctg gag 194  
 Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu  
                           50                          55                          60

atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag agc ccc gaa 242  
 Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu  
           65                          70                          75

agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa atc ttg 290  
 Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu  
   80                          85                          90

gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg gcc ctg 338  
 Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu  
   95                          100                          105                          110

tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg gag ctg 386  
 Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu  
                           115                          120                          125

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ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc cac ggc ctc 434  
 Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu  
 130 135 140  
 ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac cct gca ccc 482  
 Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro  
 145 150 155  
 cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc ccc gca ctc 530  
 Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu  
 160 165 170  
 ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc 578  
 Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser  
 175 180 185 190  
 tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga agc ccc agc 626  
 Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser  
 195 200 205  
 tac gct tcc tga agcca 643  
 Tyr Ala Ser \*

<210> 4  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser  
 1 5 10 15  
 Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro  
 20 25 30  
 Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr  
 35 40 45  
 Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg  
 50 55 60  
 Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu  
 65 70 75 80  
 Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val  
 85 90 95  
 Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly  
 100 105 110  
 Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu  
 115 120 125  
 Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu  
 130 135 140  
 His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly  
 145 150 155 160  
 Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu  
 165 170 175

20060705 04:23:00

Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp  
                   180                  185                  190  
 Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala  
                   195                  200                  205  
 Ser

<210> 5  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 5  
 agccattgat ggactcggac 20

<210> 6  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 6  
 tggcttcagg aagcgtagct 20

<210> 7  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 7  
 Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His  
   1                  5                  10                  15

<210> 8  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg  
   1                  5                  10                  15

<210> 9  
 <211> 218  
 <212> PRT  
 <213> Mus musculus

206227.5.20030304

Met	Ala	Arg	Lys	Trp	Asn	Gly	Arg	Ala	Val	Ala	Arg	Ala	Leu	Val	Leu
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Ala	Thr	Leu	Trp	Leu	Ala	Val	Ser	Gly	Arg	Pro	Leu	Ala	Gln	Gln	Ser
			20					25					30		
Gln	Ser	Val	Ser	Asp	Glu	Asp	Pro	Leu	Phe	Leu	Tyr	Gly	Trp	Gly	Lys
		35					40					45			
Ile	Thr	Arg	Leu	Gln	Tyr	Leu	Tyr	Ser	Ala	Gly	Pro	Tyr	Val	Ser	Asn
	50					55					60				
Cys	Phe	Leu	Arg	Ile	Arg	Ser	Asp	Gly	Ser	Val	Asp	Cys	Glu	Glu	Asp
65					70					75					80
Gln	Asn	Glu	Arg	Asn	Leu	Leu	Glu	Phe	Arg	Ala	Val	Ala	Leu	Lys	Thr
				85					90					95	
Ile	Ala	Ile	Lys	Asp	Val	Ser	Ser	Val	Arg	Tyr	Leu	Cys	Met	Ser	Ala
			100					105					110		
Asp	Gly	Lys	Ile	Tyr	Gly	Leu	Ile	Arg	Tyr	Ser	Glu	Glu	Asp	Cys	Thr
		115					120					125			
Phe	Arg	Glu	Glu	Met	Asp	Cys	Leu	Gly	Tyr	Asn	Gln	Tyr	Arg	Ser	Met
	130					135					140				
Lys	His	His	Leu	His	Ile	Ile	Phe	Ile	Gln	Ala	Lys	Pro	Arg	Glu	Gln
145					150					155					160
Leu	Gln	Asp	Gln	Lys	Pro	Ser	Asn	Phe	Ile	Pro	Val	Phe	His	Arg	Ser
				165					170					175	
Phe	Phe	Glu	Thr	Gly	Asp	Gln	Leu	Arg	Ser	Lys	Met	Phe	Ser	Leu	Pro
			180					185					190		
Leu	Glu	Ser	Asp	Ser	Met	Asp	Pro	Phe	Arg	Met	Val	Glu	Asp	Val	Asp
		195					200					205			
His	Leu	Val	Lys	Ser	Pro	Ser	Phe	Gln	Lys						
	210					215									

<211> 216

<212> PRT

<213> Hom

Met	Arg	Ser	Gly	Cys	Val	Val	Val	His	Val	Trp	Ile	Leu	Ala	Gly	Leu
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Trp	Leu	Ala	Val	Ala	Gly	Arg	Pro	Leu	Ala	Phe	Ser	Asp	Ala	Gly	Pro
			20					25					30		
His	Val	His	Tyr	Gly	Trp	Gly	Asp	Pro	Ile	Arg	Leu	Arg	His	Leu	Tyr
		35					40					45			
Thr	Ser	Gly	Pro	His	Gly	Leu	Ser	Ser	Cys	Phe	Leu	Arg	Ile	Arg	Ala
	50					55					60				
Asp	Gly	Val	Val	Asp	Cys	Ala	Arg	Gly	Gln	Ser	Ala	His	Ser	Leu	Leu
65				70						75				80	
Glu	Ile	Lys	Ala	Val	Ala	Leu	Arg	Thr	Val	Ala	Ile	Lys	Gly	Val	His
				85					90					95	
Ser	Val	Arg	Tyr	Leu	Cys	Met	Gly	Ala	Asp	Gly	Lys	Met	Gln	Gly	Leu
			100					105					110		
Leu	Gln	Tyr	Ser	Glu	Glu	Asp	Cys	Ala	Phe	Glu	Glu	Glu	Ile	Arg	Pro
		115					120					125			

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140  
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160  
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175  
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190  
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205  
 Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

<210> 11  
 <211> 10  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Residues which contain the anitgenic determinant  
 recognized by the myc monoclonal antibody.

<400> 11  
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu  
 1 5 10

<210> 12  
 <211> 5  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Preferred thrombin cleave site.

<400> 12  
 Leu Val Pro Arg Gly  
 1 5

<210> 13  
 <211> 10  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Residues which bind to paramagnetic streptavidin  
 beads (used for purification).

<400> 13  
 Ser Ala Trp Arg His Pro Gln Phe Gly Gly  
 1 5 10

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<210> 14  
<211> 7  
<212> PRT  
<213> Homo sapiens

<400> 14  
Arg Pro Tyr Asp Gly Tyr Asn  
1 5

<210> 15  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 15  
Leu Pro Met Leu Pro Met  
1 5

<210> 16  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 16  
Arg Pro Asp Gly Tyr Asn  
1 5

<210> 17  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 17  
His Phe Leu Pro Met Leu  
1 5

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